

FIG. 1

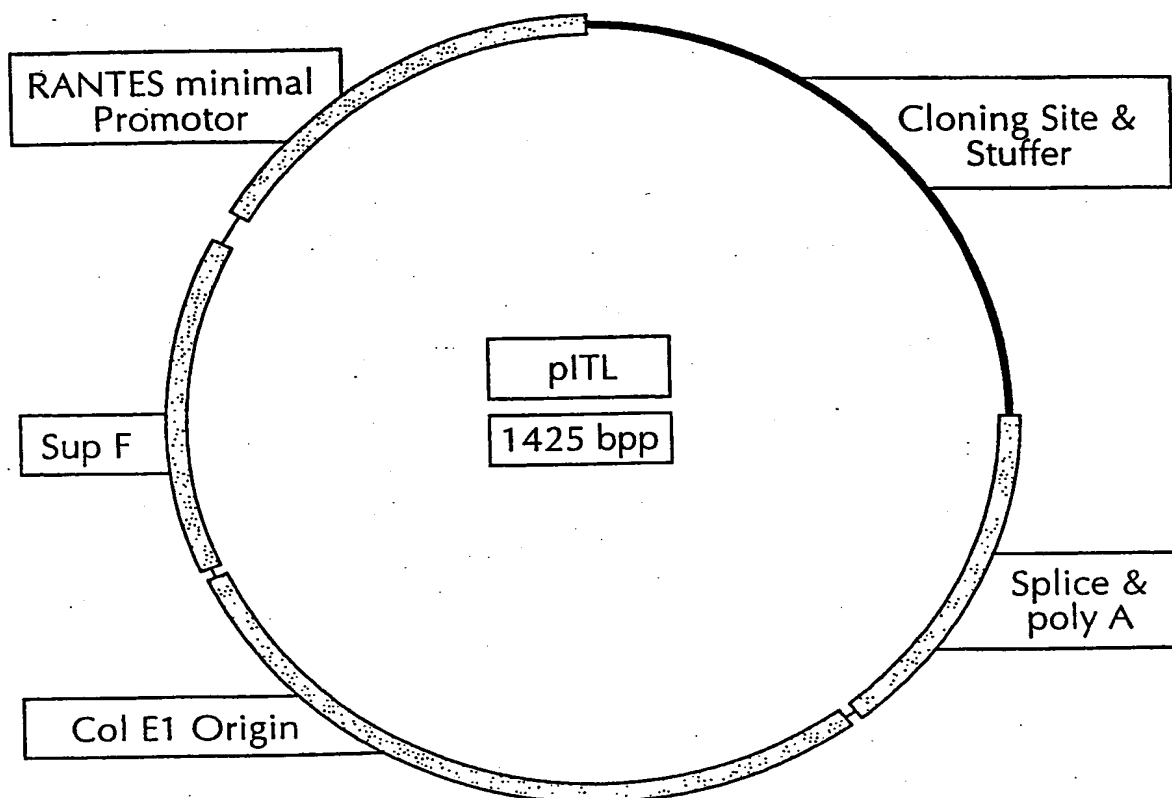


FIG. 2

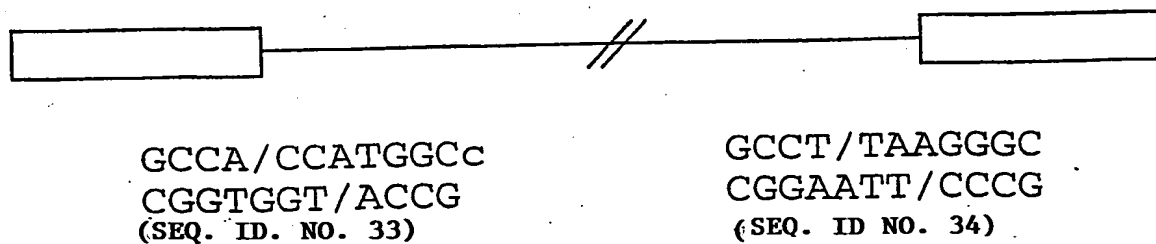




FIG. 3A

60
MRPSGTAGALLAALCPASRALEKKVCQGTSNKLTQGTFFEDHFLSLQRMFNCEVVLGNLEITYVQRYND
M---ELAAALCRWGLLLALLP-PGA-AST-VCTGTDMLKRLPASPEHLDMLRHLVQGCQVVOGNLELTYLPTNAS
57

125
LSFLKTIQEVAGYVLIANTVERIPILENLQIRGNMYENSYALAVLSNYD--AN---KT-----GLKELPMRNL
140
LSFLQDIEVQGYVLIAHNQVRQVPLQRLRIVRGTLQFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQLRSL
122
147

175
* * * * *
QEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMSMDFQNLHSGCQKCDPSCPNGS-CWGAGEENCQKLTKII
TEILKGGVLIQRNPQCYQDTILWKDIFHKNNQLALTIDTNRSRACHPCSPMCK-GSRCWGESSEDCQSLTRTV
175

289
* * * * *
CAQQCSGRCRGKSPSDCCCHNQCAAGCTGPRESDCLVCRKFRDEATCKDTPPLMLYNPTTYQMDVNPEGKYSFGA
CAGGCA-RCKGPLPTDCCCHEQCAAGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGA
295

350 *
* * * * *
YVVTDHGSCVRACGADSYEME-EDGVRKCKKCEGPCRKVCNCGIGIGEFKDSLSINATNIKHFKNCTSIGDHLHL
YLSTDVGSCTLVCPLHNQEVTAEDGTQRCCKSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFL
352

438
PVAFRGDSFTHTPPLDPQELDILKTVKEITGFLLIQAWPENRTDLHAFENLEIIRGRTKQPGQFSLAVVSLNITS
PESFDGDPASNTAPLQPEQLQVFFETLEEITGYLYISAWPDSLPLDSVFQNLQVIRGRILHNGAYSLTLQGLGISW
445



FIG. 3C

929

THQSDVWSYGVTVWELMTFGSKPYDGI PASEISSILEKGERLPQPPICTIDVYIMVKCWMIDADSRPKFRELII
THQSDVWSYGVTVWELMTFGAKPYDGI PAREIPDLLEKGERLPQPPICTIDVYIMVKCWMIDSECRPRFRELVS
940

EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGF-
EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGF-
1010
EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGF-
EFKSMARDPQRYLVIQDERMHLPSPTDSNFYRALMDEE-DMDDVVDADEYLIPOQGGF-
1040

-----SSPSTSRTPLLSSLSATSNSTVACIDRN--GLQSCPIKEDSFLQRYSSDPTGAL-T
RSSSTRSGGGDLTLGLEPSEEEAPRSLAPSEGAGSDVFDGDLGMGAAGLQSLPTHDPSPLOQRYSEDPTVPLPS
1137

1070
E-D--SIDDTFLPVPEYINQ-SVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNVTQVTCVNS
ETDGYVAPLTCSQPPEYVNPQDVRPQPPSPREGPLPAARPAAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYL
1120 1290

1150
TFDSTFLPVPEYINQ-SVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLNVTQVTCVNSTFDSP
TPQGTCSQPPEYVNPQDVRPQPPSPREGPLPAARPAAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTPQGG
1300

1210
AHWAQKGSHQ-ISL--DNPDIQ-QDFFPKEAKPNGIFKGST--AENAEYLR-VAPQSSEFIGA (SEQ. ID NO. 35)
AAP-QPHPPPAFSPAFDNLYYWDQDPPERGAPPS-TFKG-TPTAENPEYLGLDVPV (SEQ. ID NO. 36)
1255



FIG. 4A

57
MELAAALCRWGLLLALLPPGAASQVCTGTDMKRLRPASPETHLDMLRHLVQGCQVQGNLELTYLPTNASLS
MIIMELAAWCRWGFLALLPPGIAGTQVCTGTDMKRLRPASPETHLDMLRHLVQGCQVQGNLELTYVPANASLS
60

117
FLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTLQFEDNYALAVLDNGDPLNNTTPVT-GASPGGLRELQRLSLT
FLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTLQFEDKYALAVLDNRDPQDNVAASTPGRTPEGLRELQRLSLT
120

176
EILKGGVLIQRNPQLCYQDTILWKDIFHKNNQALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCA
EILKGGVLIQRNPQLCYQDMVLWKDVFRKNNQAPVDIDTNRSRACPPCAPACKDNHCWGESPEDCQILTGTICT
180

236
GGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTTFGASCV
SGCARCKGRLPTDCCHEQCAAGCTGPKHSDCLACHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTTFGASCV
240

356
TACPYNVLTSDVGSC TLVCPPLHNQEVTAEDGTORCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIF
TTCPPYNVLTSTEVGSC TLVCPPPNNQEVTAEDGTORCEKCSKPCARVCYGLGMEHLRGARAITSDNVQEFFDGCKKIF
360

416
GSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPDSLPLDLSVFQNLQVIRGRILHNGAYSLTLQ
GSLAFLPESFDGDPSSGIAPLRPEQLQVFETLEEITGYLYISAWPDSLRLDLSVFQNLRIIRGRILHDGAYSLTLQ
420

REPLACEMENT SHEET



FIG. 4C

SILRRRFTHQSDVWSYGVTVWELMTFGAKPYDGIIPAREIPDLLLEKGERLPQPPICITIDVYIMVVKCWMIDSECRP 950
SILRRRFTHQSDVWSYGVTVWEIMTFGAKPYDGIIPAREIPDLLLEKGERLPQPPICITIDVYIMVVKCWMIDSECRP 955



RFRELVSFSEFMRMARDPQRFVVIQNEIDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPOQFFCPDPAPGAGGM 1010
RFRELVSFSEFMRMARDPQRFVVIQNEIDLGPSSMDSTFYRSLLEDDDMGDLVDAEEYLVPOQFFSPDPTPGTGST 1015



VHHRSSSTRSGGDLTLGLEPSEEEAPRSLAPSEGAGSDVFDGDLGMGAAGLQSLPTHDPSPLOQRYSEDPT 1070
AHRRSSSTRSGGDLTLGLEPSEEGPRLAPSEGAGSDVFDGDLAMGVTKGLQSLSPHDLSPLOQRYSEDPT 1075



VPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVE 1130
LPLPPETDGYVAPLACSPQPEYVNQSEVQPPPLTPEGPLPPVRPAGATLERPKTLSPGKNGVVKDVFAFGGAVE 1135



NPEYLTPOGGAAPQPHPPAFSPAFDNLYYWDQDPPERGAPPSTFKGTPTAENPEYLGLDVPV (SEQ. ID NO. 36) 1255
NPEYLVREGTASPPHPPAFSPAFDNLYYWDQNSSEQPPPSNFEGTPTAENPEYLGLDVPV (SEQ. ID NO. 37) 1263